****
Reviewer Comments:
<210>   70
<211>   174
<212>   PRT
<213>   Oerskovia jenensis

<400>   70

(ERRORED PORTION SHOWN BELOW)

Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala

            115   120   125

Please remove the blank lines between the above amino acid numbers and
their respective amino acids; amino acid numbers must appear directly
below their respective amino acids.

<210>   134
<211>   340
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   synthetic

<400>   134

(ERRORED PORTION SHOWN BELOW)

Val Asn Glu Arg Gly Glu Gln Val Gln Leu Lys Gly Met Ser Ser His

        50   55   60

Please remove the blank lines between the above amino acid numbers and
their respective amino acids; amino acid numbers must appear directly
below their amino acids.

<210>   639
<211>   255
<212>   PRT
<213>   Streptogrisin C

Regarding the above "<213>" response: Reminder: per 1.823 of the
Sequence Rules, the only valid "<213>" responses are: the Genus species
of the organism, "Artificial Sequence", or "Unknown". "Artificial
Sequence" and "Unknown" require explanation in the "<220>-<223>"
section: please clearly indicate the source of the genetic material.
"Streptogrisin" also appears in the "<213>" response in subsequent
sequences.

<210>   640
<211>   185
<212>   PRT
<213>   Streptogrisin B

<400>   640

(please see below)

Ile Ser Gly Gly Asp Ala Ile Tyr Ser Ser Thr Gly Arg Cys Ser Leu
1   5   10   15
Gly Phe Asn Val Arg Ser Gly Ser Thr Tyr Tyr Phe Leu Thr Ala Gly

<pre>
          20   25   30
</pre>

"Streptogrisin" appears in the above "<213>" response. Also, please
remove the blank lines between the above amino acid numbers and their
amino acids.

<pre>
<210>   642
<211>   188
<212>   PRT
<213>   Streptogrisin D

<400>   642
</pre>

(please see below)

Gly Gln Ala Val Thr Arg Ser Gly Ser Thr Thr Gln Val His Asp Gly

<pre>
          100   105   110
</pre>

"Streptogrisin" appears in the above "<213>" response. Also, please
remove the blank lines between the above amino acid numbers and their
amino acids.

To correct the sequence listing errors noted in this report - The
recommended method for correction of errors is to access the sequence
listing working file using the software program in which the listing was
originally prepared, e.g., the project file in PatentIn, make any
necessary corrections within that program, then generate a new sequence
listing file. Use of a word processing program to correct errors
directly in the original sequence listing file is strongly discouraged,
since such programs often introduce unintended changes to the sequence
listing, rendering the listing unacceptable. When the working file or
original program is not available for correction, then use of a common
or plain text-only editor, such as NotePad, to edit the original
sequence listing file may suffice.

* *

Application No: 10576331   Version No: 3.0

Input Set:

Output Set:

Started: 2012-01-26 20:11:11.447

Finished: 2012-01-26 20:11:31.273

Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 826 ms

Total Warnings: 605

Total Errors: 28

No. of SeqIDs Defined: 656

Actual SeqID Count: 656

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 251	Found intentionally skipped sequence in SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)

Input Set:

                    Output Set:

                  Started: 2012-01-26 20:11:11.447
                 Finished: 2012-01-26 20:11:31.273
                  Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 826 ms
          Total Warnings: 605
            Total Errors: 28
    No. of SeqIDs Defined: 656
        Actual SeqID Count: 656

Error code   Error Description

W   402   Undefined organism found in <213> in SEQ ID (40)

W   213   Artificial or Unknown found in <213> in SEQ ID (45)

W   213   Artificial or Unknown found in <213> in SEQ ID (46)

W   213   Artificial or Unknown found in <213> in SEQ ID (47)

W   213   Artificial or Unknown found in <213> in SEQ ID (48)

W   213   Artificial or Unknown found in <213> in SEQ ID (49)

W   213   Artificial or Unknown found in <213> in SEQ ID (50)

W   213   Artificial or Unknown found in <213> in SEQ ID (51)

W   213   Artificial or Unknown found in <213> in SEQ ID (52)

W   402   Undefined organism found in <213> in SEQ ID (61)

W   402   Undefined organism found in <213> in SEQ ID (62)

W   402   Undefined organism found in <213> in SEQ ID (65)

W   402   Undefined organism found in <213> in SEQ ID (66)

W   402   Undefined organism found in <213> in SEQ ID (69)

W   402   Undefined organism found in <213> in SEQ ID (70)
               This error has occured more than 20 times, will not be displayed

E   355   Empty lines found between the amino acid numbering and the

E   321   No. of Bases conflict, this line has no nucleotides SEQID (70)

W   213   Artificial or Unknown found in <213> in SEQ ID (79)

W   213   Artificial or Unknown found in <213> in SEQ ID (80)

W   213   Artificial or Unknown found in <213> in SEQ ID (81)

W   213   Artificial or Unknown found in <213> in SEQ ID (82)

W   213   Artificial or Unknown found in <213> in SEQ ID (83)

Input Set:

                    Output Set:

                  Started: 2012-01-26 20:11:11.447
                 Finished: 2012-01-26 20:11:31.273
                  Elapsed: 0 hr(s) 0 min(s) 19 sec(s) 826 ms
          Total Warnings: 605
            Total Errors: 28
    No. of SeqIDs Defined: 656
      Actual SeqID Count: 656

Error code   **Error Description**

W   213   Artificial or Unknown found in <213> in SEQ ID (84)
                   This error has occured more than 20 times, will not be displayed

E   341   'Xaa' position not defined   SEQID (125)   POS (170)

E   341   'Xaa' position not defined   SEQID (125)   POS (171)

E   341   'Xaa' position not defined   SEQID (125)   POS (172)

E   341   'Xaa' position not defined   SEQID (125)   POS (173)

E   341   'Xaa' position not defined   SEQID (125)   POS (174)

E   341   'Xaa' position not defined   SEQID (125)   POS (175)

E   341   'Xaa' position not defined   SEQID (125)   POS (176)

E   341   'Xaa' position not defined   SEQID (125)   POS (177)

E   341   'Xaa' position not defined   SEQID (125)   POS (178)

E   341   'Xaa' position not defined   SEQID (125)   POS (179)

E   341   'Xaa' position not defined   SEQID (125)   POS (180)

E   341   'Xaa' position not defined   SEQID (125)   POS (181)

E   341   'Xaa' position not defined   SEQID (125)   POS (182)

E   341   'Xaa' position not defined   SEQID (125)   POS (183)

E   341   'Xaa' position not defined   SEQID (125)   POS (184)

E   341   'Xaa' position not defined   SEQID (125)   POS (185)

E   341   'Xaa' position not defined   SEQID (125)   POS (186)

E   341   'Xaa' position not defined   SEQID (125)   POS (187)

E   341   'Xaa' position not defined   SEQID (125)   POS (188)

E   341   'Xaa' position not defined   SEQID (125)   POS (189)
                   This error has occured more than 20 times, will not be displayed

Input Set:

Output Set:

Started:	2012-01-26 20:11:11.447
Finished:	2012-01-26 20:11:31.273
Elapsed:	0 hr(s) 0 min(s) 19 sec(s) 826 ms
Total Warnings:	605
Total Errors:	28
No. of SeqIDs Defined:	656
Actual SeqID Count:	656

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (134)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (640)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (642)

gcgcgctgcg cccacgacga cgccgtccgc cgttcgccgg cgtacctgcg ttggctcacc   60
acccaccaga tcgacctcca taacgaggcc gtatgaccag aaagggatct gccaccgccc   120
accagcacgc tcctaacctc cgagcaccgg cgaccgccgg gtgcgatgaa agggacgaac   180
cgagatgaca ccacgcacag tcacgcgggc cctggccgtg ccaccgcag ccgccacact   240
cctggcaggc ggcatggccg cccaggccaa cgagcccgca ccacccggga gcgcgagcgc   300
accgccacgc ctggccgaga agctcgaccc cgacctcctc gaggccatgg agcgcgacct   360
gggcctcgac gcggaggaag ccgccgccac cctggcgttc cagcacgacg cagccgagac   420
cggcgaggcc ctcgccgaag agctcgacga ggacttcgcc ggcacctggg tcgaggacga   480
cgtcctgtac gtcgccacca ccgacgagga cgccgtcgag gaggtcgagg cgaaggcgc   540
cacgccgtc accgtcgagc actccctggc cgacctcgag gcctggaaga ccgtcctcga   600
cgccgccctc gagggccacg acgacgtgcc cacctggtac gtcgacgtcc cgaccaacag   660
cgtcgtcgtc gccgtcaagg ccggagccca ggacgtcgcc gccggcctcg tcgaaggtgc   720
cgacgtcccg tccgacgccg tgaccttcgt cgagaccgac gagacccgc ggaccatgtt   780
cgacgtgatc ggcggcaacg cctacaccat cgggggcgcg agccgctgct cgatcgggtt   840
cgcggtcaac ggcgggttca tcaccgccgg ccactgcggc cgcaccggcg ccaccaccgc   900
caacccccacc gggaccttcg ccgggtccag cttcccgggc aacgactacg cgttcgtccg   960
taccgggggcc ggcgtgaacc tgctggccca ggtcaacaac tactccggtg ccgcgtcca   1020
ggtcgccggg cacaccgcgg ccccgtcgg ctcggccgtg tgccggtccg ggtcgaccac   1080
cggtggcac tgcggcacca tcactgcgct caactcctcg gtcacctacc ccgagggcac   1140
cgtccgcggc ctgatccgca ccaccgtctg cgccgagccc ggcgactccg gtggctcgct   1200

```
gctcgccggc aaccaggccc agggcgtcac gtccggcggc tccggcaact gccgcaccgg      1260
tggcaccacg ttcttccagc cggtcaaccc catcctccag gcgtacggcc tgaggatgat      1320
caccacggac tcgggcagca gcccggcccc tgcaccgacc tcctgcaccg gctacgcccg      1380
caccttcacc gggaccctcg cggccggccg ggccgccgcc cagcccaacg ggtcctacgt      1440
gcaggtcaac cggtccggga cccacagcgt gtgcctcaac gggccctccg gtgcggactt      1500
cgacctctac gtgcagcgct ggaacggcag ctcctgggtg accgtcgccc agagcacctc      1560
ccccggctcc aacgagacca tcacctaccg cggcaacgcc ggctactacc gctacgtggt      1620
caacgccgcg tccggctccg gtgcctacac catggggctc accctcccct gacgtagcgc      1680
```

<210>   2
<211>   1488
<212>   DNA
<213>   Cellulomonas strain 69B4

<400>   2
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atgacaccac gcacagtcac gcgggccctg gccgtggcca ccgcagccgc cacactcctg        60
gcaggcggca tggccgccca ggccaacgag cccgcaccac ccgggagcgc gagcgcaccg       120
ccacgcctgg ccgagaagct cgaccccgac ctcctcgagg ccatggagcg cgacctgggc       180
ctcgacgcgg aggaagccgc cgccaccctg gcgttccagc acgacgcagc cgagaccggc       240
gaggccctcg ccgaagagct cgacgaggac ttcgccggca cctgggtcga ggacgacgtc       300
ctgtacgtcg ccaccaccga cgaggacgcc gtcgaggagg tcgagggcga aggcgccacg       360
gccgtcaccg tcgagcactc cctggccgac ctcgaggcct ggaagaccgt cctcgacgcc       420
gccctcgagg ccacgacga cgtgcccacc tggtacgtcg acgtcccgac caacagcgtc       480
gtcgtcgccg tcaaggccgg agcccaggac gtcgccgccg gcctcgtcga aggtgccgac       540
gtcccgtccg acgccgtgac cttcgtcgag accgacgaga ccccgcggac catgttcgac       600
gtgatcggcg gcaacgccta caccatcggg gggcgcagcc gctgctcgat cgggttcgcg       660
gtcaacggcg ggttcatcac cgccggccac tgcggccgca ccggcgccac caccgccaac       720
cccaccggga ccttcgccgg gtccagcttc ccgggcaacg actacgcgtt cgtccgtacc       780
ggggccggcg tgaacctgct ggcccaggtc aacaactact ccggtggccg cgtccaggtc       840
gccgggcaca ccgcggcccc cgtcggctcg gccgtgtgcc ggtccgggtc gaccaccggg       900
tggcactgcg gcaccatcac tgcgctcaac tcctcggtca cctaccccga gggcaccgtc       960
cgcggcctga tccgcaccac cgtctgcgcc gagcccggcg actccggtgg ctcgctgctc      1020
gccggcaacc aggcccaggg cgtcacgtcc ggcggctccg gcaactgccg caccggtggc      1080
accacgttct tccagccggt caaccccatc ctccaggcgt acggcctgag gatgatcacc      1140
acggactcgg gcagcagccc ggcccctgca ccgacctcct gcaccggcta cgcccgcacc      1200
ttcaccggga ccctcgcggc cggccgggcc gccgcccagc caacgggtc ctacgtgcag      1260
gtcaaccggt ccgggaccca gagcgtgtgc ctcaacgggc cctccggtgc ggacttcgac      1320
ctctacgtgc agcgctggaa cggcagctcc tgggtgaccg tcgcccagag cacctccccc      1380
ggctccaacg agaccatcac ctaccgcggc aacgccggct actaccgcta cgtggtcaac      1440
gccgcgtccg gctccggtgc ctacaccatg gggctcaccc tccctga               1488
```

<210>   3
<211>   1404
<212>   DNA
<213>   Cellulomonas spp.

<400>   3
```
aacgagcccg caccacccgg gagcgcgagc gcaccgccac gcctggccga gaagctcgac        60
cccgacctcc tcgaggccat ggagcgcgac ctgggcctcg acgcggagga agccgccgcc       120
accctggcgt tccagcacga cgcagccgag accggcgagg ccctcgccga agagctcgac       180
gaggacttcg ccggcacctg ggtcgaggac gacgtcctgt acgtcgccac caccgacgag       240
gacgccgtcg aggaggtcga gggcgaaggc gccacggccg tcaccgtcga gcactccctg       300
gccgacctcg aggcctggaa gaccgtcctc gacgccgccc tcgagggcca cgacgacgtg       360
cccacctggt acgtcgacgt cccgaccaac agcgtcgtcg tcgccgtcaa ggccggagcc       420
caggacgtcg ccgccggcct cgtcgaaggt gccgacgtcc gtccgacgc cgtgaccttc       480
gtcgagaccg acgagacccc gcggaccatg ttcgacgtga tcggcggcaa cgcctacacc       540
atcggggggc gcagccgctg ctcgatcggg ttcgcggtca acggcgggtt catcaccgcc       600
```

```
ggccactgcg gccgcaccgg cgccaccacc gccaacccca ccgggacctt cgccgggtcc        660
agcttcccgg gcaacgacta cgcgttcgtc cgtaccgggg ccggcgtgaa cctgctggcc        720
caggtcaaca actactccgg tggccgcgtc caggtcgccg ggcacaccgc ggcccccgtc        780
ggctcggccg tgtgccggtc cgggtcgacc accgggtggc actgcggcac catcactgcg        840
ctcaactcct cggtcaccta ccccgagggc accgtccgcg gcctgatccg caccaccgtc        900
tgcgccgagc ccggcgactc cggtggctcg ctgctcgccg gcaaccaggc ccaggcgtc          960
acgtccggcg gctccggcaa ctgccgcacc ggtggcacca cgttcttcca gccggtcaac       1020
cccatcctcc aggcgtacgg cctgaggatg atcaccacgg actcgggcag cagcccggcc       1080
cctgcaccga cctcctgcac cggctacgcc cgcaccttca ccgggaccct cgcggccggc       1140
cgggccgccg cccagcccaa cgggtcctac gtgcaggtca accggtccgg gacccacagc       1200
gtgtgcctca acgggccctc cggtgcggac ttcgacctct acgtgcagcg ctggaacggc       1260
agctcctggg tgaccgtcgc ccagagcacc tcccccggct ccaacgagac catcacctac       1320
cgcggcaacg ccggctacta ccgctacgtg gtcaacgccg gtccggctc cggtgcctac        1380
accatggggc tcaccctccc ctga                                              1404


<210>  4
<211>  567
<212>  DNA
<213>  Cellulomonas spp.


<400>  4
ttcgacgtga tcggcggcaa cgcctacacc atcgggggggc gcagccgctg ctcgatcggg         60
ttcgcggtca acggcgggtt catcaccgcc ggccactgcg gccgcaccgg cgccaccacc        120
gccaacccca ccgggacctt cgccgggtcc agcttcccgg gcaacgacta cgcgttcgtc        180
cgtaccgggg ccggcgtgaa cctgctggcc caggtcaaca actactccgg tggccgcgtc        240
caggtcgccg ggcacaccgc ggcccccgtc ggctcggccg tgtgccggtc cgggtcgacc        300
accgggtggc actgcggcac catcactgcg ctcaactcct cggtcaccta ccccgagggc        360
accgtccgcg gcctgatccg caccaccgtc tgcgccgagc ccggcgactc cggtggctcg        420
ctgctcgccg gcaaccaggc ccaggcgtc acgtccggcg gctccggcaa ctgccgcacc         480
ggtggcacca cgttcttcca gccggtcaac cccatcctcc aggcgtacgg cctgaggatg        540
atcaccacgg actcgggcag cagcccg                                            567


<210>  5
<211>  83
<212>  DNA
<213>  Cellulomonas strain 69B4


<400>  5
atgacaccac cacagtcacg cgggccctgg ccgtggccac cgcagccgcc acactcctgg         60
caggcggcat ggccgcccag gcc                                                83


<210>  6
<211>  495
<212>  PRT
<213>  Cellulomonas strain 69B4


<400>  6


Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
1               5                   10                  15
Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala Asn Glu Pro Ala
            20                  25                  30
Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala Glu Lys Leu Asp
        35                  40                  45
Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly Leu Asp Ala Glu
    50                  55                  60
Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala Ala Glu Thr Gly
```

```
          65                      70                      75                      80
Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala Gly Thr Trp Val
                    85                      90                      95
Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu Asp Ala Val Glu
                    100                     105                     110
Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val Glu His Ser Leu
        115                     120                     125
Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala Ala Leu Glu Gly
        130                     135                     140
His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro Thr Asn Ser Val
145                     150                     155                     160
Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala Ala Gly Leu Val
                    165                     170                     175
Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe Val Glu Thr Asp
                    180                     185                     190
Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly Asn Ala Tyr Thr
                    195                     200                     205
Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala Val Asn Gly Gly
        210                     215                     220
Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn
225                     230                     235                     240
Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala
                    245                     250                     255
Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala Gln Val Asn Asn
                    260                     265                     270
Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr Ala Ala Pro Val
        275                     280                     285
Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
        290                     295                     300
Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro Glu Gly Thr Val
305                     310                     315                     320
Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
                    325                     330                     335
Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly
        340                     345                     350
Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe Gln Pro Val Asn
        355                     360                     365
Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr Thr Asp Ser Gly
        370                     375                     380
Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly Tyr Ala Arg Thr
385                     390                     395                     400
Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala Gln Pro Asn Gly
                    405                     410                     415
Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser Val Cys Leu Asn
                    420                     425                     430
Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln Arg Trp Asn Gly
        435                     440                     445
Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro Gly Ser Asn Glu
        450                     455                     460
Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg Tyr Val Val Asn
465                     470                     475                     480
Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu Thr Leu Pro
                    485                     490                     495


<210>   7
<211>   467
<212>   PRT
```

<212> Cellulomonas strain 69B4

<400> 7

```
Asn Glu Pro Ala Pro Pro Gly Ser Ala Ser Ala Pro Pro Arg Leu Ala
1               5                   10                  15
Glu Lys Leu Asp Pro Asp Leu Leu Glu Ala Met Glu Arg Asp Leu Gly
            20                  25                  30
Leu Asp Ala Glu Glu Ala Ala Ala Thr Leu Ala Phe Gln His Asp Ala
        35                  40                  45
Ala Glu Thr Gly Glu Ala Leu Ala Glu Glu Leu Asp Glu Asp Phe Ala
    50                  55                  60
Gly Thr Trp Val Glu Asp Asp Val Leu Tyr Val Ala Thr Thr Asp Glu
65                  70                  75                  80
Asp Ala Val Glu Glu Val Glu Gly Glu Gly Ala Thr Ala Val Thr Val
                85                  90                  95
Glu His Ser Leu Ala Asp Leu Glu Ala Trp Lys Thr Val Leu Asp Ala
            100                 105                 110
Ala Leu Glu Gly His Asp Asp Val Pro Thr Trp Tyr Val Asp Val Pro
        115                 120                 125
Thr Asn Ser Val Val Val Ala Val Lys Ala Gly Ala Gln Asp Val Ala
    130                 135                 140
Ala Gly Leu Val Glu Gly Ala Asp Val Pro Ser Asp Ala Val Thr Phe
145                 150                 155                 160
Val Glu Thr Asp Glu Thr Pro Arg Thr Met Phe Asp Val Ile Gly Gly
                165                 170                 175
Asn Ala Tyr Thr Ile Gly Gly Arg Ser Arg Cys Ser Ile Gly Phe Ala
            180                 185                 190
Val Asn Gly Gly Phe Ile Thr Ala Gly His Cys Gly Arg Thr Gly Ala
            195                 200                 205
Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala Gly Ser Ser Phe Pro Gly
    210                 215                 220
Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala Gly Val Asn Leu Leu Ala
225                 230                 235                 240
Gln Val Asn Asn Tyr Ser Gly Gly Arg Val Gln Val Ala Gly His Thr
                245                 250                 255
Ala Ala Pro Val Gly Ser Ala Val Cys Arg Ser Gly Ser Thr Thr Gly
            260                 265                 270
Trp His Cys Gly Thr Ile Thr Ala Leu Asn Ser Ser Val Thr Tyr Pro
    275                 280                 285
Glu Gly Thr Val Arg Gly Leu Ile Arg Thr Thr Val Cys Ala Glu Pro
    290                 295                 300
Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly Asn Gln Ala Gln Gly Val
305                 310                 315                 320
Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Phe
                325                 330                 335
Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu Arg Met Ile Thr
            340                 345                 350
Thr Asp Ser Gly Ser Ser Pro Ala Pro Ala Pro Thr Ser Cys Thr Gly
        355                 360                 365
Tyr Ala Arg Thr Phe Thr Gly Thr Leu Ala Ala Gly Arg Ala Ala Ala
    370                 375                 380
Gln Pro Asn Gly Ser Tyr Val Gln Val Asn Arg Ser Gly Thr His Ser
385                 390                 395                 400
Val Cys Leu Asn Gly Pro Ser Gly Ala Asp Phe Asp Leu Tyr Val Gln
            405                 410                 415
Arg Trp Asn Gly Ser Ser Trp Val Thr Val Ala Gln Ser Thr Ser Pro
```

Gly Ser Asn Glu Thr Ile Thr Tyr Arg Gly Asn Ala Gly Tyr Tyr Arg
        435   440   445
Tyr Val Val Asn Ala Ala Ser Gly Ser Gly Ala Tyr Thr Met Gly Leu
    450   455   460
Thr Leu Pro
465

<210>   8
<211>   189
<212>   PRT
<213>   Cellulomonas strain 69B4

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Cys Ser Ile Gly Phe Ala Val Asn Gly Gly Phe Ile Thr Ala Gly His
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Cys Gly Arg Thr Gly Ala Thr Thr Ala Asn Pro Thr Gly Thr Phe Ala
        35   40   45
Gly Ser Ser Phe Pro Gly Asn Asp Tyr Ala Phe Val Arg Thr Gly Ala
    50   55   60
Gly Val Asn Leu Leu Ala Gln Val Asn Asn Tyr Ser Gly Gly Arg Val
65   70   75   80
Gln Val Ala Gly His Thr Ala Ala Pro Val Gly Ser Ala Val Cys Arg
                85   90   95
Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Thr Ala Leu Asn
            100   105   110
Ser Ser Val Thr Tyr Pro Glu Gly Thr Val Arg Gly Leu Ile Arg Thr
        115   120   125
Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Leu Leu Ala Gly
    130   135   140
Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr
145   150   155   160
Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr
                165   170   175
Gly Leu Arg Met Ile Thr Thr Asp Ser Gly Ser Ser Pro
            180   185

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<213>   Cellulomonas strain 69B4

<400>   9

Met Thr Pro Arg Thr Val Thr Arg Ala Leu Ala Val Ala Thr Ala Ala
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Ala Thr Leu Leu Ala Gly Gly Met Ala Ala Gln Ala
            20   25

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